



SEQUENCE LISTING

<110> JENSEN, Martin Roland et al.
<120> NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID
<130> 3631-0107P
<140> 09/785,215
<141> 2001-02-20
<160> 19
<170> PatentIn version 3.1

<210> 1
<211> 2313
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2313)
<223>

<220>
<221> misc_feature
<222> (2098)..(2169)
<223> nucleotides encoding transmembrane region

<220>
<221> misc_feature
<222> (2014)..(2313)
<223> Nucleotides encoding C-100

<220>
<221> misc_feature
<222> (2016)..(2144)
<223> Abeta 42/43

<220>
<221> misc_feature
<222> (2014)..(2142)
<223> Abeta 42/43

<400> 1
atg ctg ccc ggt ttg gca ctg ctc ctg ctg gcc gcc tgg acg gct cgg
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

48

gaa gcc gat gat gac gag gac gat gag gat ggt gat gag gta gag gaa	768
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu	
245 250 255	
gag gct gag gaa ccc tac gaa gaa gcc aca gag aga acc acc agc att	816
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile	
260 265 270	
gcc acc acc acc acc acc acc aca gag tct gtg gaa gag gtg gtt cga	864
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg	
275 280 285	
gag gtg tgc tct gaa caa gcc gag acg ggg ccg tgc cga gca atg atc	912
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile	
290 295 300	
tcc cgc tgg tac ttt gat gtg act gaa ggg aag tgt gcc cca ttc ttt	960
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe	
305 310 315 320	
tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac	1008
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr	
325 330 335	
tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act	1056
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr	
340 345 350	
acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca	1104
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala	
355 360 365	
gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat	1152
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp	
370 375 380	
gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc	1200
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala	
385 390 395 400	
aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca	1248
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala	
405 410 415	
gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc	1296
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile	
420 425 430	
cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac	1344
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn	
435 440 445	
gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg	1392
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met	
450 455 460	

ctc Leu 465	aat Asn	gac Asp	cgc Arg	cgc Arg	cgc Arg	ctg Leu	gcc Ala	ctg Leu	gag Glu	aac Asn	tac Tyr	atc Ile	acc Thr	gct Ala	ctg Leu	1440
					470					475					480	
cag Gln	gct Ala	gtt Val	cct Pro	cct Pro	cgg Arg	cct Pro	cgt Arg	cac His	gtg Val	ttc Phe	aat Asn	atg Met	cta Leu	aag Lys	aag Lys	1488
				485					490					495		
tat Tyr	gtc Val	cgc Arg	gca Ala	gaa Glu	cag Gln	aag Lys	gac Asp	aga Arg	cag Gln	cac His	acc Thr	cta Leu	aag Lys	cat His	ttc Phe	1536
			500					505					510			
gag Glu	cat His	gtg Val	cgc Arg	atg Met	gtg Val	gat Asp	ccc Pro	aag Lys	aaa Lys	gcc Ala	gct Ala	cag Gln	atc Ile	cgg Arg	tcc Ser	1584
		515					520					525				
cag Gln	gtt Val	atg Met	aca Thr	cac His	ctc Leu	cgt Arg	gtg Val	att Ile	tat Tyr	gag Glu	cgc Arg	atg Met	aat Asn	cag Gln	tct Ser	1632
	530					535					540					
ctc Leu 545	tcc Ser	ctg Leu	ctc Leu	tac Tyr	aac Asn	gtg Val	cct Pro	gca Ala	gtg Val	gcc Ala	gag Glu	gag Glu	att Ile	cag Gln	gat Asp	1680
					550					555					560	
gaa Glu	gtt Val	gat Asp	gag Glu	ctg Leu	ctt Leu	cag Gln	aaa Lys	gag Glu	caa Gln	aac Asn	tat Tyr	tca Ser	gat Asp	gac Asp	gtc Val	1728
				565					570					575		
ttg Leu	gcc Ala	aac Asn	atg Met	att Ile	agt Ser	gaa Glu	cca Pro	agg Arg	atc Ile	agt Ser	tac Tyr	gga Gly	aac Asn	gat Asp	gct Ala	1776
			580					585					590			
ctc Leu	atg Met	cca Pro	tct Ser	ttg Leu	acc Thr	gaa Glu	acg Thr	aaa Lys	acc Thr	acc Thr	gtg Val	gag Glu	ctc Leu	ctt Leu	ccc Pro	1824
		595					600					605				
gtg Val	aat Asn	gga Gly	gag Glu	ttc Phe	agc Ser	ctg Leu	gac Asp	gat Asp	ctc Leu	cag Gln	ccg Pro	tgg Trp	cat His	tct Ser	ttt Phe	1872
	610					615					620					
ggg Gly 625	gct Ala	gac Asp	tct Ser	gtg Val	cca Pro	gcc Ala	aac Asn	aca Thr	gaa Glu	aac Asn	gaa Glu	gtt Val	gag Glu	cct Pro	gtt Val	1920
					630					635					640	
gat Asp	gcc Ala	cgc Arg	cct Pro	gct Ala	gcc Ala	gac Asp	cga Arg	gga Gly	ctg Leu	acc Thr	act Thr	cga Arg	cca Pro	ggt Gly	tct Ser	1968
				645					650					655		
ggg Gly	ttg Leu	aca Thr	aat Asn	atc Ile	aag Lys	acg Thr	gag Glu	gag Glu	atc Ile	tct Ser	gaa Glu	gtg Val	aag Lys	atg Met	gat Asp	2016
			660					665					670			
gca Ala	gaa Glu	ttc Phe	cga Arg	cat His	gac Asp	tca Ser	gga Gly	tat Tyr	gaa Glu	gtt Val	cat His	cat His	caa Gln	aaa Lys	ttg Leu	2064
		675					680					685				

gtg	ttc	ttt	gca	gaa	gat	gtg	ggt	tca	aac	aaa	ggt	gca	atc	att	gga	2112
Val	Phe	Phe	Ala	Glu	Asp	Val	Gly	Ser	Asn	Lys	Gly	Ala	Ile	Ile	Gly	
690						695					700					

ctc	atg	gtg	ggc	ggt	gtt	gtc	ata	gcg	aca	gtg	atc	gtc	atc	acc	ttg	2160
Leu	Met	Val	Gly	Gly	Val	Val	Ile	Ala	Thr	Val	Ile	Val	Ile	Thr	Leu	
705					710					715					720	

gtg	atg	ctg	aag	aag	aaa	cag	tac	aca	tcc	att	cat	cat	ggt	gtg	gtg	2208
Val	Met	Leu	Lys	Lys	Lys	Gln	Tyr	Thr	Ser	Ile	His	His	Gly	Val	Val	
			725						730					735		

gag	gtt	gac	gcc	gct	gtc	acc	cca	gag	gag	cgc	cac	ctg	tcc	aag	atg	2256
Glu	Val	Asp	Ala	Ala	Val	Thr	Pro	Glu	Glu	Arg	His	Leu	Ser	Lys	Met	
			740					745					750			

cag	cag	aac	ggc	tac	gaa	aat	cca	acc	tac	aag	ttc	ttt	gag	cag	atg	2304
Gln	Gln	Asn	Gly	Tyr	Glu	Asn	Pro	Thr	Tyr	Lys	Phe	Phe	Glu	Gln	Met	
		755					760					765				

cag	aac	tag														2313
Gln	Asn															
	770															

<210> 2
 <211> 770
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg
1				5					10					15	

Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro
			20					25					30		

Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
		35					40					45			

Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
50						55					60				

Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
65					70					75					80

Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
				85					90					95	

100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 3
<211> 45
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(45)
<223> DNA encoding P2 epitope

<400> 3
cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 4
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 4
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 5
<211> 63
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(63)
<223> DNA encoding P30 epitope

<400> 5
ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

gct agc cac ctg gaa 63
Ala Ser His Leu Glu
20

<210> 6
<211> 21

<212> PRT
 <213> Clostridium tetani
 <400> 6

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15

Ala Ser His Leu Glu
 20

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer targeted to the pAB1 plasmid

<400> 7
 caactcagct tcctttcggg c 21

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer targeted to the pAB1 plasmid

<400> 8
 agatctcgat cccgcgaaat t 21

<210> 9
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer that encodes the human abeta-43 fragment with E. coli
 optimised codons

<400> 9
 atggatgcag aattccgtca cgactccggt tacgaagttc accaccagaa actgggttttc 60
 ttcgcagaag atgttggttc caacaaaggt gcaatcatcg gtctgatggt tggcggtggt 120
 gttatcgcga cctag 135

<210> 10
 <211> 31

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer derived from SEQ ID NO:9

 <400> 10
 gccggccatg gatgcagaat tccgtcacga c 31

<210> 11
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer derived from SEQ ID NO:9

 <400> 11
 gccggaagct tctaggtcgc gataacaaca ccgccaacc 39

<210> 12
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer encoding the P2 epitope

 <400> 12
 ccggcaagct tctacagctc ggtgataccg atgaatttgg agttagcttt gatgtactgg 60
 gtcgcgataa caacaccgcc aacc 84

<210> 13
 <211> 101
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer derived from the pAB1 plasmid

 <400> 13
 gccggccatg gggtttcaaca acttcaccgt tagcttctgg ctgcgtgttc cgaaagttag 60
 cgcgagccac ctggaagatg cagaattccg tcacgactcc g 101

<210> 14
 <211> 172
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer derived from the pAB2 plasmid

<400> 14

gggccaaagct tggatccggt cgcgataaca acaccgcca ccatcagacc gatgattgca 60

cctttgttgg aaccaacatc ttctgcgaag aaaaccagtt tctggtggtg aacttcgtaa 120

cgggagtcgt gacggaactc tgcattccagc tcggtgatac cgatgaattt gg 172

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer derived from the pAB3 plasmid

<400> 15

ctggaagatg cagagttccg tcacgactcc 30

<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer derived from the pAB3 plasmid

<400> 16

gcgccggatc cttcaacaac ttcaccgtta gcttc 35

<210> 17

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence, used as an example for how to calculate sequence identity, has 75% sequence identity with SEQ ID NO:18

<400> 17

agtcagtc 8

<210> 18

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence, used as an example for how to calculate sequence identity, has 75% sequence identity with SEQ ID NO:17

<400> 18
aatcaatc

8

<210> 19
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial T-cell epitope capable of binding to a large portion
of MHC Class II molecules in a variety of animals

<400> 19

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10